IFWO

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RAW SEQUENCE LISTING                       DATE: 09/17/2004
PATENT APPLICATION:  US/10/755,466         TIME: 10:41:44

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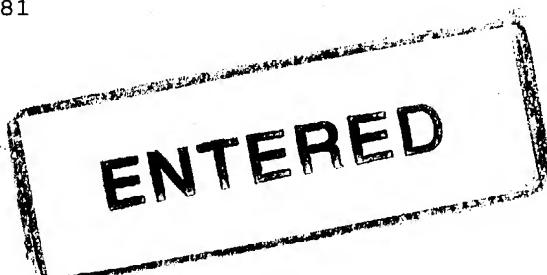
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 1 <110> APPLICANT: HIDAKA , Jun et al.
 2 <120> TITLE OF INVENTION: RECOMBINANT HUMAN SM-11044-BINDING RECEPTOR PROTEINS
EXHIBITING LIGAND-
 3       BINDING ACTIVITIES, AND THEIR USES
 4 <130> FILE REFERENCE: 0020-4827P
 5 <140> CURRENT APPLICATION NUMBER: US/10/755,466
 6 <141> CURRENT FILING DATE: 2004-01-13
 7 <150> PRIOR APPLICATION NUMBER: US/09/786,681
 8 <151> PRIOR FILING DATE: 2001-04-30
 9 <160> NUMBER OF SEQ ID NOS: 7
10 <170> SOFTWARE: PatentIn version 3.0
12 <210> SEQ ID NO: 1
13 <211> LENGTH: 2072
14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
16 <220> FEATURE:
17 <221> NAME/KEY: CDS
18 <222> LOCATION: (49)..(1794)
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20       ggatccacta gtaacggccg ccagtgtgct ggaattctgc agatctag atg cat gct      57
21                                                            Met His Ala
22                                                            1
23       cga gcg gcc gcc gcg ctg tgg ctg ctg ctg ctg ctg ctg ccc cgg acc     105
24       Arg Ala Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu Pro Arg Thr
25           5                   10                  15
26       cgg gcg gac gag cac gaa cac acg tat caa gat aaa gag gaa gtt gtc     153
27       Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu Glu Val Val
28       20                  25                  30                  35
29       tta tgg atg aat act gtt ggg ccc tac cat aat cgt caa gaa aca tat     201
30       Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln Glu Thr Tyr
31                       40                  45                  50
32       aag tac ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa agt atc agt     249
33       Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys Ser Ile Ser
34                   55                  60                  65
35       cat tac cat gaa act ctg gga gaa gca ctt caa ggg gtt gaa ttg gaa     297
36       His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val Glu Leu Glu
37               70                  75                  80
38       ttt agt ggt ctg gat att aaa ttt aaa gat gat gtg atg cca gcc act     345
39       Phe Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met Pro Ala Thr
40           85                  90                  95
41       tac tgt gaa att gat tta gat aaa gaa aag aga gat gca ttt gta tat     393
42       Tyr Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala Phe Val Tyr
43       100                 105                 110                 115
44       gcc ata aaa aat cat tac tgg tac cag atg tac ata gat gat tta cca     441
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45        Ala Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp Asp Leu Pro
46                            120                 125                 130
47        ata tgg ggt att gtt ggt gag gct gat gaa aat gga gaa gat tac tat    489
48        Ile Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu Asp Tyr Tyr
49                            135                 140                 145
50        ctt tgg acc tat aaa aaa ctt gaa ata ggt ttt aat gga aat cga att    537
51        Leu Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly Asn Arg Ile
52                    150                 155                 160
53        gtt gat gtt aat cta act agt gaa gga aag gtg aaa ctg gtt cca aat    585
54        Val Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu Val Pro Asn
55                165                 170                 175
56        act aaa atc cag atg tca tat tca gta aaa tgg aaa aag tca gat gtg    633
57        Thr Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys Ser Asp Val
58        180                 185                 190                 195
59        aaa ttt gaa gat cga ttt gac aaa tat ctt gat ccg tcc ttt ttt caa    681
60        Lys Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser Phe Phe Gln
61                            200                 205                 210
62        cat cgg att cat tgg ttt tca att ttc aac tcc ttc atg atg gtg atc    729
63        His Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met Met Val Ile
64                            215                 220                 225
65        ttc ttg gtg ggc tta gtt tca atg att tta atg aga aca tta aga aaa    777
66        Phe Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr Leu Arg Lys
67                    230                 235                 240
68        gat tat gct cgg tac agt aaa gag gaa gaa atg gat gat atg gat aga    825
69        Asp Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp Met Asp Arg
70                245                 250                 255
71        gac cta gga gat gaa tat gga tgg aaa cag gtg cat gga gat gta ttt    873
72        Asp Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly Asp Val Phe
73        260                 265                 270                 275
74        aga cca tca agt cac cca ctg ata ttt tcc tct ctg att ggt tct gga    921
75        Arg Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile Gly Ser Gly
76                            280                 285                 290
77        tgt cag ata ttt gct gtg tct ctc atc gtt att att gtt gca atg ata    969
78        Cys Gln Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val Ala Met Ile
79                    295                 300                 305
80        gaa gat tta tat act gag agg gga tca atg ctc agt aca gcc ata ttt   1017
81        Glu Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr Ala Ile Phe
82                310                 315                 320
83        gtc tat gct gct acg tct cca gtg aat ggt tat ttt gga gga agt ctg   1065
84        Val Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly Gly Ser Leu
85                325                 330                 335
86        tat gct aga caa gga gga agg aga tgg ata aag cag atg ttt att ggg   1113
87        Tyr Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met Phe Ile Gly
88        340                 345                 350                 355
89        gca ttc ctt atc cca gct atg gtg tgt ggc act gcc ttc ttc atc aat   1161
90        Ala Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe Phe Ile Asn
91                            360                 365                 370
92        ttc ata gcc att tat tac cat gct tca aga gcc att cct ttt gga aca   1209
93        Phe Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro Phe Gly Thr
```

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94                375              380              385
95     atg gtg gcc gtt tgt tgc atc tgt ttt ttt gtt att ctt cct cta aat   1257
96     Met Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu Pro Leu Asn
97                390              395              400
98     ctt gtt ggt aca ata ctt ggc cga aat ctg tca ggt cag ccc aac ttt   1305
99     Leu Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln Pro Asn Phe
100            405              410              415
101     cct tgt cgt gtc aat gct gtg cct cgt cct ata ccg gag aaa aaa tgg  1353
102     Pro Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu Lys Lys Trp
103    420              425              430                  435
104    ttc atg gag cct gcg gtt att gtt tgc ctg ggt gga att tta cct ttt   1401
105    Phe Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile Leu Pro Phe
106                440              445              450
107    ggt tca atc ttt att gaa atg tat ttc atc ttc acg tct ttc tgg gca   1449
108    Gly Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser Phe Trp Ala
109            455              460              465
110    tat aag atc tat tat gtc tat ggc ttc atg atg ctg gtg ctg gtt atc   1497
111    Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val Leu Val Ile
112            470              475              480
113    ctg tgc att gtg act gtc tgt gtg act att gtg tgc aca tat ttt cta   1545
114    Leu Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr Tyr Phe Leu
115            485              490              495
116    cta aat gca gaa gat tac cgg tgg caa tgg aca agt ttt ctc tct gct   1593
117    Leu Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe Leu Ser Ala
118    500              505              510                  515
119    gca tca act gca atc tat gtt tac atg tat tcc ttt tac tac tat ttt   1641
120    Ala Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr Tyr Tyr Phe
121            520              525              530
122    ttc aaa aca aag atg tat ggc tta ttt caa aca tca ttt tac ttt gga   1689
123    Phe Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe Tyr Phe Gly
124            535              540              545
125    tat atg gcg gta ttt agc aca gcc ttg ggg ata atg tgt gga gcg att   1737
126    Tyr Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys Gly Ala Ile
127            550              555              560
128    ggt tac atg gga aca agt gcc ttt gtc cga aaa atc tat act aat gtg   1785
129    Gly Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr Thr Asn Val
130            565              570              575
131    aaa att gac tagagaccca agaaacctg gaactttgga tcaatttctt           1834
132    Lys Ile Asp
133    580
134    tttcataggg gtggaacttg cacagcaaaa acaaacaaac gcaagaagag atttgggctt  1894
135    taactttttt tttttttttt tttttttttt tttttttttt tacgaatgag gcaatttatt  1954
136    aacccagcat ggtttgttct aatgcttctt gttggcagct gccacctgtc cggcgattct  2014
137    gtccagatct ctttgtccct gaggtgtcag tttgcggccg ctcgagcatg catctaga    2072
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 582
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
143 <400> SEQUENCE: 2
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144        Met His Ala Arg Ala Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu
145         1           5               10             15
146        Pro Arg Thr Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu
147                20              25             30
148        Glu Val Val Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln
149                35              40             45
150        Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys
151         50              55             60
152        Ser Ile Ser His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val
153         65              70             75             80
154        Glu Leu Glu Phe Ser Gly Leu Asp Ile Lys Phe Lys Asp Asp Val Met
155                85              90             95
156        Pro Ala Thr Tyr Cys Glu Ile Asp Leu Asp Lys Glu Lys Arg Asp Ala
157                100             105            110
158        Phe Val Tyr Ala Ile Lys Asn His Tyr Trp Tyr Gln Met Tyr Ile Asp
159                115             120            125
160        Asp Leu Pro Ile Trp Gly Ile Val Gly Glu Ala Asp Glu Asn Gly Glu
161                130             135            140
162        Asp Tyr Tyr Leu Trp Thr Tyr Lys Lys Leu Glu Ile Gly Phe Asn Gly
163         145             150            155            160
164        Asn Arg Ile Val Asp Val Asn Leu Thr Ser Glu Gly Lys Val Lys Leu
165                165             170            175
166        Val Pro Asn Thr Lys Ile Gln Met Ser Tyr Ser Val Lys Trp Lys Lys
167                180             185            190
168        Ser Asp Val Lys Phe Glu Asp Arg Phe Asp Lys Tyr Leu Asp Pro Ser
169                195             200            205
170        Phe Phe Gln His Arg Ile His Trp Phe Ser Ile Phe Asn Ser Phe Met
171                210             215            220
172        Met Val Ile Phe Leu Val Gly Leu Val Ser Met Ile Leu Met Arg Thr
173         225             230            235            240
174        Leu Arg Lys Asp Tyr Ala Arg Tyr Ser Lys Glu Glu Glu Met Asp Asp
175                245             250            255
176        Met Asp Arg Asp Leu Gly Asp Glu Tyr Gly Trp Lys Gln Val His Gly
177                260             265            270
178        Asp Val Phe Arg Pro Ser Ser His Pro Leu Ile Phe Ser Ser Leu Ile
179                275             280            285
180        Gly Ser Gly Cys Gln Ile Phe Ala Val Ser Leu Ile Val Ile Ile Val
181                290             295            300
182        Ala Met Ile Glu Asp Leu Tyr Thr Glu Arg Gly Ser Met Leu Ser Thr
183         305             310            315            320
184        Ala Ile Phe Val Tyr Ala Ala Thr Ser Pro Val Asn Gly Tyr Phe Gly
185                325             330            335
186        Gly Ser Leu Tyr Ala Arg Gln Gly Gly Arg Arg Trp Ile Lys Gln Met
187                340             345            350
188        Phe Ile Gly Ala Phe Leu Ile Pro Ala Met Val Cys Gly Thr Ala Phe
189                355             360            365
190        Phe Ile Asn Phe Ile Ala Ile Tyr Tyr His Ala Ser Arg Ala Ile Pro
191                370             375            380
192        Phe Gly Thr Met Val Ala Val Cys Cys Ile Cys Phe Phe Val Ile Leu
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193          385                     390                     395                     400
194          Pro Leu Asn Leu Val Gly Thr Ile Leu Gly Arg Asn Leu Ser Gly Gln
195                          405                     410                     415
196          Pro Asn Phe Pro Cys Arg Val Asn Ala Val Pro Arg Pro Ile Pro Glu
197                          420                     425                     430
198          Lys Lys Trp Phe Met Glu Pro Ala Val Ile Val Cys Leu Gly Gly Ile
199                          435                     440                     445
200          Leu Pro Phe Gly Ser Ile Phe Ile Glu Met Tyr Phe Ile Phe Thr Ser
201                  450                     455                     460
202          Phe Trp Ala Tyr Lys Ile Tyr Tyr Val Tyr Gly Phe Met Met Leu Val
203          465                     470                     475                     480
204          Leu Val Ile Leu Cys Ile Val Thr Val Cys Val Thr Ile Val Cys Thr
205                          485                     490                     495
206          Tyr Phe Leu Leu Asn Ala Glu Asp Tyr Arg Trp Gln Trp Thr Ser Phe
207                  500                     505                     510
208          Leu Ser Ala Ala Ser Thr Ala Ile Tyr Val Tyr Met Tyr Ser Phe Tyr
209                  515                     520                     525
210          Tyr Tyr Phe Phe Lys Thr Lys Met Tyr Gly Leu Phe Gln Thr Ser Phe
211                  530                     535                     540
212          Tyr Phe Gly Tyr Met Ala Val Phe Ser Thr Ala Leu Gly Ile Met Cys
213          545                     550                     555                     560
214          Gly Ala Ile Gly Tyr Met Gly Thr Ser Ala Phe Val Arg Lys Ile Tyr
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217                          580
219     <210> SEQ ID NO: 3
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221     <212> TYPE: DNA
222     <213> ORGANISM: Homo sapiens
223     <220> FEATURE:
224     <221> NAME/KEY: CDS
225     <222> LOCATION: (11)..(1747)
226     <400> SEQUENCE: 3
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228                     Met Ala Ala Ala Ala Leu Trp Leu Leu Leu Leu Leu Leu
229                      1               5                       10
230          ccc cgg acc cgg gcg gac gag cac gaa cac acg tat caa gat aaa gag          97
231          Pro Arg Thr Arg Ala Asp Glu His Glu His Thr Tyr Gln Asp Lys Glu
232               15                  20                      25
233          gaa gtt gtc tta tgg atg aat act gtt ggg ccc tac cat aat cgt caa          145
234          Glu Val Val Leu Trp Met Asn Thr Val Gly Pro Tyr His Asn Arg Gln
235          30                  35                      40                      45
236          gaa aca tat aag tac ttt tca ctt cca ttc tgt gtg ggg tca aaa aaa          193
237          Glu Thr Tyr Lys Tyr Phe Ser Leu Pro Phe Cys Val Gly Ser Lys Lys
238                          50                      55                      60
239          agt atc agt cat tac cat gaa act ctg gga gaa gca ctt caa ggg gtt          241
240          Ser Ile Ser His Tyr His Glu Thr Leu Gly Glu Ala Leu Gln Gly Val
241                  65                      70                      75
242          gaa ttg gaa ttt agt ggt ctg gat att aaa ttt aaa gat gat gtg atg          289
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Input Set : **N:\Crf3\RULE60\10755466.raw**
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Seq#:7; Line(s) 442

VERIFICATION SUMMARY   DATE: 09/17/2004
PATENT APPLICATION: **US/10/755,466**   TIME: 10:41:45

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